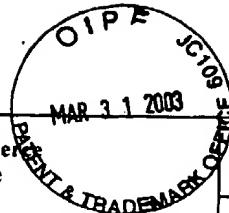


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Serial No.
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Applicant
Andrey Rzhetsky et al.

Filing Date
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U.S. PATENT DOCUMENTS

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FOREIGN PATENT DOCUMENT

	Document No.	Date	Country	Class	SubClass	Translator Yes No

OTHER DOCUMENTS (including Author, Title Date, Pertinent Pages, Etc.)

A	Ballinger CA et al., 1999, "Identification of CHIP, a novel tetratricopeptide repeat-containing protein that interacts with heat shock proteins and negatively regulates chaperone functions," <i>Mol Cell. Biol.</i> 19:4535-4545.
AB	Barabasi and Albert, 1999, "Emergence of scaling in random networks," <i>Science</i> 286:509-512.
AB	Enright AJ et al., 1999, "Protein interaction maps for complete genomes based on gene fusion events," <i>Nature</i> 402:86-90.
AB	Marcotte EM et al., 1999, "Detecting protein function and protein-protein interactions from genome sequences," <i>Science</i> 285:751-753.
AB	Ruecknagel KP et al., 1999, Dihydrolipoamide S-Succinyltransferase Precursor, Accession XUBYSD (gi 2144399)

NY02:433911.1

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Date Considered

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<i>A</i>	Bailey et al., 1998, "Analysis of EST-driven gene annotation in human genomic sequence," <i>Genome Research</i> 8:362-376.
	Bono et al., 1998, "Reconstruction of amino acid biosynthesis pathways from the complete genome sequence," <i>Genome Res.</i> 8:203-210.
	Friedman C et al., 1998, "Evaluating natural language processing," <i>Methods of Information in Medicine</i> 37:334-44.
	Goto S et al., 1998, "LIGAND:chemical database for enzymes reactions," <i>Nucleic Acid Research</i> 14:591-599.
	Grundy, 1998, "Homology detection via family pairwise search," <i>J. Computational Biology</i> 5:479-491.
	Hu et al., 1998, "WD-40 repeat region regulates Apaf-1 self-association and procaspase-9 activation," <i>J. Biol. Chem.</i> 273:33489-33494.
	Sonnhammer ELL et al., 1998, "Pfam:multiple sequence alignments and HMM profiles of protein domains," <i>Nucleic Acids Research</i> 26(1):320-322.
	Wu SK et al., 1998, "Molecular role for the Rab binding platform of guanine nucleotide dissociation inhibitor in endoplasmic reticulum to golgi transport," <i>J. Biol. Chem.</i> 273:26931-26938.
	Yuan et al., 1998, "Towards detection of orthologues in sequence databases," <i>Bioinformatics</i> 14:285-289.
	Altschul et al., 1997, "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs," <i>Nucleic Acids Research</i> 25:3389-3402.
	Attwood TK et al., 1997, "The PRINTS database of protein fingerprints:a novel information resource for computational molecular biology," <i>J. Chem. Inf. Comput. Sci.</i> 37:417-424.
<i>A</i>	Cserzo M et al., 1997, "Prediction of transmembrane α -helices in prokaryotic membrane proteins:the dense alignment surface method," <i>Protein Engineering</i> 10:673-676.
<i>A</i>	Goto et al., 1997, "Organizing and computing metabolic pathway data in terms of binary relations," <i>Pac. Symp. Biocomput.</i> 2:175-186.

NY02:433911.1

Examiner

Date Considered

4/28/04

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U.S. PATENT AND TRADEMARK OFFICE

Grundy et al., 1997, "Hidden Markov model analysis of motifs in steroid dehydrogenases and their homologs," *Biochem Biophys. Res. Commun.* 231(3):760-766.

Grundy WN et al., 1997, "Meta-MEME: motif-based hidden Markov models of protein families," *CABIOS* 13:397-406.

Mushegian AR et al., 1997, "Positionally cloned human disease genes:patterns of evolutionary conservation and functional motifs," *Proc. Natl. Acad Sci. USA* 94:5831-5836.

Neuwald, 1997, "Extracting protein alignment models from the sequence database," *Nucleic Acids Research* 25:1665-1677.

Pearson, 1997, "Identifying distantly related protein sequences," *CABIOS*, 13:325-332;

Pena et al., 1997, "Stress-induced apoptosis and the sphingomyelin pathway," *Biochem Pharmacol.*, 53:615-621.

Rogers MA et al., 1997, "Sequences and differential expression of the three novel human type II hair keratins," *Differentiation* 61:187-194.

Selkov, E et al., 1997, "The metabolic pathway collection: an update," *Nucleic Acids Research* 25:37-38.

Sharkey et al., 1997, "Hox genes in evolution: protein surfaces and paralog groups," *TIG* 13:145-151.

Skvorak AB et al., 1997, "An ancient conserved gene expressed in the human inner ear: identification, expression analysis, and chromosome mapping of human and mouse antiquitin (ATQ1)," *Genomics* 46:191-199.

Sonnhammer ELL et al., 1997, Pfam:A comprehensive database of protein domains families based on seed alignments, *Proteins Structure Function and Genetics* 28:405-420.

NY02:433911.1

Examiner

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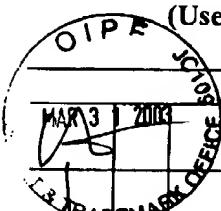
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Group
1631



Tatusov RL et al., 1997, "A genomic perspective on protein families," *Science* 278:631-637.

Boskovic J et al., 1996, Transcription Factor GRF10, Accession A25872 (gi|82888).

Bucher et al., 1996, "A flexible motif search technique based on generalized profiles," *Comput. Chem.*, 20:3-23.

Felsenstein J, 1996, "Inferring phylogenies from protein sequence by parsimony, distance, and likelihood means," *Methods in Enzymology* 266:418-427.

Gilks WR et al., eds., 1996, *Markov Chain Monte Carlo Practice*, Chapman & Hall/CRC, New York.

Gustafsson C et al., 1996, "Identification of new RNA modifying enzymes by iterative genome search using known modifying enzymes as probes," *Nucleic Acids Research* 24:3756-3762.

Jain NL et al., 1996, "Identification of suspected tuberculosis patients based on natural language processing of chest radiograph reports," *Proc. AMIA Annu Fall Symp* 542-546.

James CM et al., 1996, Cell Division Control Protein CDC43, Accession RGBY43 (gi|2144611).

Koonin EV et al., 1996, "Protein sequence comparison at sequence scale," *Methods in Enzymology* 266:295-323.

Mathews S et al., 1996, "The phytochrome family in grasses (Poaceae): A phlogeny and evidence that grasses have a subset of the loci found in dicot angiosperms," *Mol. Biol. Evol.*, 13:1141-1150

Miklos GLG, et al., 1996, "The role of the genome project in determining gene function:insights from model organisms," *Cell* 86:521-529.

Selkov et al., 1996, "The metabolic pathway collection from EMP: the enzymes and metabolic pathways database," *Nucleic Acids Research* 24:26-28.

Wu CH et al., 1996, "Motif identification neural design for rapid and sensitive protein family search," *Comput. Appl. Biosci* 12:109-118.

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Group
1631

Bailey et al. 1995, "The value of prior knowledge in discovering motifs," *Proc. Int Conf Intell Sys Biol.* 3:21-29.

Boldin et al., 1995, "A novel protein that interacts with the death domain of Fas./APO1 contains a sequence motif related to the death domain," *J Biol Chem.* 270:7795-8.

Friedman et al., 1995, "Natural language processing in an operational clinical information system, *Natural Language Engineering*, 1:83-108.

Green PJ, 1995, "Reversible Markov chain Monte Carlo computation and Bayesian model determination," *Biometrika* 82:711-732.

Hofmann et al., 1995, "The death domain motif found in Fas(Apo-1) and TNF receptor is present in proteins involved in apoptosis and axonal guidance," *FEBS Lett.* 371:321-3.

Hripcak G et al., "Unlocking clinical data from narrative reports: a study of natural language processing," 1995, *Ann. Intern Med.* 122:681-688.

Hurlin PJ., 1995, "Mad3 and Mad4:novel Max-interacting transcriptional repressors that suppress c-myc dependent transformation and are expressed during neural and epidermal differentiation," *EMBO* 14:5646-59.

Neuwald AF et al., 1995, "Gibbs motif sampling:detection of bacterial outer membrane protein repeats," *Protein Sci.* 4:1618-1632.

Purnelle B et al., 1995, Pre-mRNA Splicing Factor PRP21, Accession S23553 (gi|280467)

Yang Z et al., 1995, "Maximum likelihood trees from DNA sequences: A peculiar statistical estimation problem," *Syst. Biol.* 44:384-399.

Zweigenbaum et al., 1995, "A multi-lingual architecture for building a normalised conceptual representation from medical language," *AMIA*, 357-361

NY02:433911.1

Examiner

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4/28/04

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Group
1631

MAP 3 - 2003	Claverie, 1994, "Some useful statistical properties of position-weight matrices," <i>Comput. Chem.</i> , 18:287-94.
U.S. TRADEMARK OFFICE	Churcher C, 1994, Dihydrolipoamide Dehydrogenase Precursor, Accession A30151 (gi 82983)
	Contreras R et al., 1994, Hypothetical Protein YBL067C, Accession S45803 (gi 626480)
	Entian KD et al., 1994, Omnipotent Suppressor Protein SUP45, Accession S46014 (gi 626763)
	Gaillon L et al., 1994, Transcription Factor BAS1, Accession A40083 (gi 101447)
	Hamlyn N et al., 1994, Oxoglutarate Dehydrogenase Precursor, Accession DEBY (gi 1070439)
	Kazic 1994, "Representation of biochemistry for modeling organisms," In: <u>Molecular Modeling: From Virtual Tools to Real Problems</u> , Kumasinski, T. and Lieberman, M.N. (Eds.), American Chemical Society, Washington, D.C. pp. 486-494.
	Kazic, 1994, "Biochemical databases: Challenges and opportunities," In: <u>New Data Challenges in Our Information Age</u> Glaeser, P.S. and Millward, M.T.L. (Eds.). Proceedings of the Thirteenth International CODATA Secretariat, Paris pp. C133-C140.
	Krogh et al., 1994, "Hidden Markov Models in computational biology, applications to protein modeling," <i>J. Mol. Biol.</i> 235:1501-1531.
	Lenert et al., 1994, "Automated linkage of free-text description of patients with a practice guideline," <i>AMIA</i> , 274-278.
	Murphy L et al., 1994, Suppressor 2 Protein, Accession EFBY52 (gi 72877)
	Rieger M, 1994, Protein Farnesyltransferase Chain RAM2, Accession P29703 (gi 266880)
<i>[Signature]</i>	Tatusov RL et al., 1994, "Detection of conserved segments in proteins: Iterative scanning of sequence databases with alignment blocks," <i>Proc. Natl Acad. Sci. USA</i> 91:12091-12095.

NY02:433911.1

Examiner

Date Considered

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Orrego et al., 1993, "A local alignment method for protein structure motifs," *J Mol Biol* 233(3):488-497.

Ullrich O et al., 1993, "Rab GDP dissociation inhibitor as a general regulator for the membrane association of Rab proteins," *J. Biol. Chem.* 268:18143-18150.

Venezia, 1993, "Rapid motif compliance scoring with match weight sets," *Comput Appl Biosci*, 9:65-9.

Baud et al., 1992, "Natural language processing and semantical representation of medical texts," *Meth. Info. Med.*, 31:117-125.

Peitgen HO; Juregens H; Saupe D, 1992, *Chaos and Fractals: New Frontiers of Science*, Springer Verlag, New York

Hirst et al., 1991, "Prediction of ATP-binding motifs: a comparison of a perceptron-type neural network and a consensus sequence method," *Prot Eng*, 4:615-623.

Altschul et al., 1990, "Basic local alignment search tool," *J. Mol. Biol.* 215:403-410.

Goldman N, 1990, "Maximum likelihood inference of phylogenetic trees, with special references to a poisson process model of DNA substitution and to parsimony analyses," *Syst. Zoo.* 39:345-361.

Haug et al., 1990, "Computerized extraction of coded findings from free-text radiologic reports," *Radiology*, 174:543-548.

Karlin S et al., 1990, "Methods for assessing the statistical significance of the molecular sequences features by using general scoring schemes," *Proc. Natl. Acad. Sci. USA* 87:2264-2268

Pamilo P et al., 1988, "Relationship between gene tree and species trees," *Mol. Biol. Evol.* 5:568-583.

Saitou N, 1987, "The neighbor-joining method : A new method for reconstructing phylogenetic trees," *Mol. Biol. Evol.* 4:406-425.

Fitch WM, 1974, "Evolutionary trees with minimum nucleotide replacements from amino acid sequences," *J. Mol. Evol.* 3:263-278.

NY02:433911.1

Examiner

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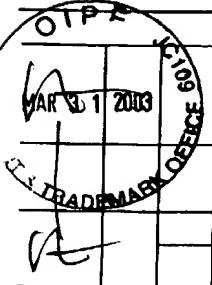
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Felsenstein J, 1978, "Cases in which parsimony or compatibility methods will be positively misleading," *Syst. Zool.*, 27:401-410.

Fitch WM, 1970, "Distinguishing homologous from analogous proteins," *Syst. Zool.*, 19:99-113.

Hastings, 1970, "Monte Carlo sampling methods using Markov chains and their applications," *Biometrika* 57:97-109.

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